

7.0

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 5, 2005, 09:16:41 ; Search time 1002.05 Seconds  
(without alignments)  
967.120 Million cell updates/sec

Title: US-09-943-115A-9

Perfect score: 20

Sequence: 1 catgccctgtctctcttca 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

1: gb.ba.\*

2: gb.htg.\*

3: gb.in.\*

4: gb.om.\*

5: gb.ov.\*

6: gb.pat.\*

7: gb.ph.\*

8: gb.pl.\*

9: gb.pr.\*

10: gb.ro.\*

11: gb.ste.\*

12: gb.sv.\*

13: gb.un.\*

14: gb.vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	AX421261 Sequence
2	20	100.0	1001	6	CQ853861 Sequence
3	20	100.0	1013	9	AF181105 Homo sapi
4	20	100.0	1345	6	AR142139 Sequence
5	20	100.0	1345	6	AR142140 Sequence
6	20	100.0	1345	6	BD222974 CYP3A4 NF
7	20	100.0	1345	6	BD222975 CYP3A4 NF
8	20	100.0	1345	6	CQ776018 Sequence
9	20	100.0	1345	6	CQ790615 Sequence
10	20	100.0	1345	6	AR222893 Sequence
11	20	100.0	1345	6	AX421253 Sequence
12	20	100.0	1345	6	HUMCYP3A4
13	20	100.0	6101	6	CQ806643 Sequence
14	20	100.0	11374	9	AF185589 Homo sapi
15	20	100.0	96960	6	AX706964 Sequence
16	20	100.0	96960	6	AX707894 Sequence
17	20	100.0	123778	9	AC069294 Homo sapi
18	20	100.0	174832	9	AF280107 Homo sapi
19	19	95.0	176766	2	AC121258 Mus muscu

20	18.4	92.0	141296	9	AL354714
21	18.4	92.0	150348	2	AC127477
22	18.4	92.0	158146	9	AC005076
23	18.4	92.0	168338	2	AC143421
24	18.4	92.0	170470	9	AC146392
25	18.4	92.0	185053	2	AC109288
26	18.4	90.0	4300	5	FRU243429
27	18.4	90.0	13293	5	FRU243430
28	18.4	90.0	164331	2	AC118869
29	18.4	90.0	232188	10	AL672055
30	18.4	90.0	233316	2	AC145168
31	18.4	90.0	253507	2	AC096421
32	18.4	90.0	263603	2	AC111291
33	18.4	90.0	269409	2	AC130995
34	17.4	87.0	35550	9	AC105386
35	17.4	87.0	68868	2	AC101770
36	17.4	87.0	82309	9	AC138136
37	17.4	87.0	85166	2	AC008617
38	17.4	87.0	100000	9	AP000074
39	17.4	87.0	109770	2	AC073763
40	17.4	87.0	110000	1	AP006841
41	17.4	87.0	110000	2	AC109085
42	17.4	87.0	110000	2	AC073763
43	17.4	87.0	110720	2	AC138189
44	17.4	87.0	110804	9	AC004748
45	17.4	87.0	127361	9	AC007283
46	17.4	87.0	143669	9	AP006307
47	17.4	87.0	149436	2	AC118970
48	17.4	87.0	153384	2	AC092518
49	17.4	87.0	158822	2	AC136174
50	17.4	87.0	161498	9	AC113376
51	17.4	87.0	166452	9	AC090453
52	17.4	87.0	168063	8	CNS07108
53	17.4	87.0	168136	10	AC117803
54	17.4	87.0	170607	10	AC133650
55	17.4	87.0	175440	10	AC125374
56	17.4	87.0	176032	2	BX510656
57	17.4	87.0	176542	2	AC025036
58	17.4	87.0	176598	2	AC146834
59	17.4	87.0	182281	2	AC150213
60	17.4	87.0	187359	10	AC087183
61	17.4	87.0	190646	2	BX649483
62	17.4	87.0	191104	10	AC123860
63	17.4	87.0	191191	10	AL663083
64	17.4	87.0	195954	10	AC102154
65	17.4	87.0	196550	2	AC118178
66	17.4	87.0	198057	2	AC073719
67	17.4	87.0	204324	2	AC150724
68	17.4	87.0	212007	10	AL935060
69	17.4	87.0	222439	10	AC124505
70	17.4	87.0	226601	10	AC122863
71	17.4	87.0	231443	2	AC073691
72	17.4	87.0	235418	2	AC126665
73	17.4	87.0	242810	2	AC129394
74	17.4	87.0	245342	2	AC130961
75	17.4	87.0	245539	2	AC121656
76	17.4	87.0	257954	10	AC122547
77	17.4	87.0	286014	2	AC112125
78	17.4	85.0	24775	3	CBC27H6
79	17.4	85.0	25172	9	AF284446
80	17.4	85.0	66715	2	AC102943
81	17.4	85.0	94056	9	AL133192
82	17.4	85.0	110000	2	AC106983
83	17.4	85.0	133608	2	AC117753
84	17.4	85.0	139222	2	AC135090
85	17.4	85.0	148601	2	AC149650
86	17.4	85.0	159243	2	AC135660
87	17.4	85.0	167697	9	AC015660
88	17.4	85.0	174265	2	AL772355
89	17.4	85.0	178254	9	AL731541
90	17.4	85.0	185872	9	AC091144
91	17.4	85.0	189649	2	AC139641
92	17.4	85.0	191082	2	AC141066

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OM nucleic - nucleic search, using sw model

Run on: July 5, 2005, 09:16:41 ; Search time 2642.05 Seconds  
(without alignments)  
288.142 Million cell updates/sec

Title: US-09-943-115a-9  
Perfect score: 20  
Sequence: 1 catgccctgtctctcttta 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database :

EST:\*

- 1: gb\_est1:\*
- 2: gb\_est2:\*
- 3: gb\_hlc:\*
- 4: gb\_est3:\*
- 5: gb\_est4:\*
- 6: gb\_est5:\*
- 7: gb\_est6:\*
- 8: gb\_gss1:\*
- 9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	19.4	95.0	575	8	AZ718060 RPCI-24-8
C 2	18.4	92.0	544	6	CB089186 Qs06a07.b
C 3	18.0	90.0	691	6	CB525676 UI-N-FY0-
C 4	18.0	90.0	769	8	CC320522 TAM32-27E
C 5	17.4	87.0	361	2	AW050373 UI-M-BHL-
C 6	17.4	87.0	382	7	CV514313 TgRSTzyr0
C 7	17.4	87.0	387	6	BY649264 BY649264
C 8	17.4	87.0	402	8	AQ035986 CIT-HSP-2
C 9	17.4	87.0	420	2	BE591420 WHE1659-1
C 10	17.4	87.0	424	2	BE689585
C 11	17.4	87.0	446	2	BF457758 UI-M-B21-
C 12	17.4	87.0	489	8	AY127534 AY127534
C 13	17.4	87.0	501	6	CD544848 B0261D03-
C 14	17.4	87.0	534	1	AJ685383 AJ685383
C 15	17.4	87.0	536	4	BI114963 602862776
C 16	17.4	87.0	542	1	AJ774072
C 17	17.4	87.0	547	2	AW536535
C 18	17.4	87.0	595	6	CB523135 UI-N-GK0-
C 19	17.4	87.0	600	4	BI985487 3142-35 M
C 20	17.4	87.0	632	5	BP305637 BP305637
C 21	17.4	87.0	650	9	AG167439 Pan trogl
C 22	17.4	87.0	679	2	BB667251 BB667251
C 23	17.4	87.0	724	7	CB814986 AGENCOURT
C 24	17.4	87.0	770	5	BQ804532 WHE3555_G

C 25	17.4	87.0	783	9	BX999657
C 26	17.4	87.0	879	9	CL305570
C 27	17.4	87.0	904	9	AG538427
C 28	17.4	87.0	948	7	CN505617
C 29	17.4	87.0	1066	8	CC283327
C 30	17.4	87.0	1157	8	CC250523
C 31	17.4	87.0	1168	8	CC285993
C 32	17.4	87.0	371	8	BH302715
C 33	17.4	87.0	459	1	AI190664
C 34	17.4	87.0	476	8	BZ692740
C 35	17.4	87.0	542	8	AQ974551 RPCI-23-3
C 36	17.4	87.0	581	5	BP321928 BP321928
C 37	17.4	87.0	647	8	BH026130 RPCI-24-3
C 38	17.4	87.0	690	8	BH386665 AG-ND-103
C 39	17.4	87.0	768	8	AZ189167 SP-1013-B
C 40	17.4	87.0	910	2	BE543546 601070515
C 41	17.4	87.0	916	5	BQ735524 AGENCOURT
C 42	17.4	87.0	1020	8	CC221604 CH261-3P2
C 43	17.4	87.0	272	2	BH384218 BH384218
C 44	17.4	87.0	352	6	CD923261 G750-107H
C 45	17.4	87.0	367	5	BY078014 BY078014
C 46	17.4	87.0	377	9	CL401130 ZMMBB040
C 47	17.4	87.0	379	8	AQ093947 HS 2199 A
C 48	17.4	87.0	388	4	BJ283135 BJ283135
C 49	17.4	87.0	401	1	AA881144 VZ06H08.r
C 50	17.4	87.0	405	9	CE335380 t19f-g88-
C 51	17.4	87.0	445	8	AQ179569 HS-3179 A
C 52	17.4	87.0	448	1	AJ679242 AJ679242
C 53	17.4	87.0	448	1	AA261020 mz77e08.r
C 54	17.4	87.0	462	4	BJ278077 BJ278077
C 55	17.4	87.0	470	1	AA102305 Z19A04.r
C 56	17.4	87.0	471	2	BB796564 BB796564
C 57	17.4	87.0	477	8	AZ238179 RPCI-23-8
C 58	17.4	87.0	480	1	AJ693148 AJ693148
C 59	17.4	87.0	482	9	CL323902 RPCI44_46
C 60	17.4	87.0	487	4	BJ283117 BJ283117
C 61	17.4	87.0	492	8	AQ997051 RPCI-23-3
C 62	17.4	87.0	497	7	CF516018 CAP0002-1
C 63	17.4	87.0	498	8	AQ618705 HS 5169 A
C 64	17.4	87.0	501	6	CA702181 wdKic.pk0
C 65	17.4	87.0	509	4	BJ278058 BJ278058
C 66	17.4	87.0	522	5	BX529662 BX529662
C 67	17.4	87.0	529	7	CO123197 GR_EB05D
C 68	17.4	87.0	541	8	BH278914 CH230-17J
C 69	17.4	87.0	543	8	AZ089486 RPCI-23-3
C 70	17.4	87.0	550	7	CF983433 mak20a07.
C 71	17.4	87.0	561	7	CO886111 BovGen.16
C 72	17.4	87.0	578	6	CD988377 G174-1080
C 73	17.4	87.0	580	5	BX114808 BX114808
C 74	17.4	87.0	600	5	BU918109 5013-47 M
C 75	17.4	87.0	634	2	BB048419 BB048419
C 76	17.4	87.0	637	5	BQ999225 QG21H13.
C 77	17.4	87.0	644	8	BH334589 CH230-596
C 78	17.4	87.0	651	7	CN604713 USDA_FP_1
C 79	17.4	87.0	663	9	CE275558 t19f-g88-
C 80	17.4	87.0	668	1	AL700041 DKFZp686A
C 81	17.4	87.0	676	6	CD689711 EST6234 h
C 82	17.4	87.0	680	8	BZ905557 CH240_27F
C 83	17.4	87.0	693	3	CC552009 CH240_437
C 84	17.4	87.0	699	6	CD988376 G174_1080
C 85	17.4	87.0	733	7	CV100178 FAMU_USDA
C 86	17.4	87.0	735	2	BB619744 BB619744
C 87	17.4	87.0	745	6	CD903449 G356-110G
C 88	17.4	87.0	753	9	CC580305 CH240_374
C 89	17.4	87.0	765	3	AG604596 Mus_muscul
C 90	17.4	87.0	769	9	CR166627 Forward s
C 91	17.4	87.0	772	9	CL654808 PRI0121c
C 92	17.4	87.0	779	9	CC509150 CH240_351
C 93	17.4	87.0	784	8	BZ265120 BZ265120
C 94	17.4	87.0	787	6	CB347189 CAB2SG000
C 95	17.4	87.0	801	6	CB346615 CAB2SG000
C 96	17.4	87.0	807	9	AG509509 Mus_muscul
C 97	17.4	87.0	811	9	CR084805 Forward s

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OM nucleic - nucleic search, using sw model

Run on: July 5, 2005, 09:16:41 ; Search time 346.667 Seconds  
(without alignments)  
341.524 Million cell updates/sec

Title: US-09-943-115a-9

Perfect score: 20

Sequence: 1 catgccctgtctctcttta 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : N\_Geneseq\_16Dec04:\*

- 1: Geneseq19808:\*
- 2: Geneseq19908:\*
- 3: Geneseq20008:\*
- 4: Geneseq20018:\*
- 5: Geneseq20028:\*
- 6: Geneseq20038:\*
- 7: Geneseq20048:\*
- 8: Geneseq20058:\*
- 9: Geneseq20068:\*
- 10: Geneseq20078:\*
- 11: Geneseq20088:\*
- 12: Geneseq20098:\*
- 13: Geneseq20108:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	6	Abk68753 PCR prime
2	20	100.0	1001	13	Adc81033 Human phe
3	20	100.0	1345	2	Aax28296 Human CYP
4	20	100.0	1345	3	Aaz57019 Nucleic a
5	20	100.0	1345	3	Aaz57020 Nucleic a
6	20	100.0	1345	6	Abk68745 5'-flanki
7	20	100.0	1345	12	Adj84441 Human phe
8	20	100.0	6101	13	Adc89077 Human CYP
9	20	100.0	12983	8	Aad51239 Human CYP
10	20	100.0	13035	8	Aad51997 Human CYP
11	20	100.0	15185	8	Aad52000 Human CYP
12	20	100.0	39071	12	Adm97420 prostate
13	20	100.0	96960	8	Acfc62734 Cancer ba
14	20	100.0	96960	8	Adb20849 WRP1 base
15	20	100.0	96960	10	Adb87938 Human UGT
16	20	100.0	96960	10	Adb96921 Human MDR
17	20	100.0	96960	10	Adb92112 Human MDR
18	20	100.0	123785	10	Abk77171 DNA seque
19	17.4	87.0	38358	4	Aak73535 Human imm
20	17	85.0	1025	6	Abk35006 Human cdn

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OM nucleic - nucleic search, using sw model

Run on: July .5, 2005, 09:16:41 ; Search time 101.538 Seconds  
(without alignments)  
322.297 Million cell updates/sec

Title: US-09-943-115A-9

Perfect score: 20

Sequence: 1 catgcccgtctctctctta 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents NA.\*  
1: /cgm2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
2: /cgm2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgm2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgm2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgm2\_6/ptodata/1/ina/PTUS\_COMB.seq:\*  
6: /cgm2\_6/ptodata/1/ina/backfiles.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	1345	3	US-09-372-339-1
2	20	100.0	1345	3	US-09-372-339-2
3	20	100.0	1345	3	US-09-144-367-3
4	20	100.0	31197	4	US-09-949-016-12963
5	20	100.0	103934	4	US-09-949-016-14433
6	18.4	92.0	35064	4	US-09-949-016-12778
7	18.4	92.0	35065	4	US-09-949-016-13196
8	17	85.0	601	4	US-09-949-016-15959
9	17	85.0	29172	4	US-09-949-016-15520
10	16.8	84.0	192	4	US-08-956-171E-1551
11	16.8	84.0	192	4	US-08-781-986A-1551
12	16.8	84.0	397	4	US-09-621-976-17859
13	16.8	84.0	72278	4	US-09-949-016-16113
14	16.8	84.0	421118	4	US-09-949-016-16297
15	16.4	82.0	601	4	US-09-949-016-17834
16	16.4	82.0	2905	4	US-09-620-312D-45
17	16.4	82.0	319608	4	US-09-539-333D-1
18	16.4	82.0	319608	4	US-09-679-409-1
19	16.4	82.0	390890	4	US-09-949-016-14720
20	16	80.0	363	1	US-08-349-492B-1
21	16	80.0	363	2	US-08-798-143-1
22	16	80.0	363	5	PCT-US95-15484-1
23	16	80.0	577	4	US-09-016-434-47
24	16	80.0	577	5	PCT-US95-07171-1
25	15.8	79.0	601	4	US-09-949-016-37725
26	15.8	79.0	601	4	US-09-949-016-37726
27	15.8	79.0	601	4	US-09-949-016-38228

c 28	15.8	79.0	601	4	US-09-949-016-76282	Sequence 76282, A
c 29	15.8	79.0	601	4	US-09-949-016-76283	Sequence 76283, A
c 30	15.8	79.0	601	4	US-09-949-016-78795	Sequence 78795, A
c 31	15.8	79.0	601	4	US-09-949-016-78796	Sequence 78796, A
c 32	15.8	79.0	601	4	US-09-949-016-113084	Sequence 113084, A
c 33	15.8	79.0	601	4	US-09-949-016-146833	Sequence 146833, A
c 34	15.8	79.0	601	4	US-09-949-016-159915	Sequence 159915, A
c 35	15.8	79.0	601	4	US-09-949-016-159936	Sequence 159936, A
c 36	15.8	79.0	601	4	US-09-949-016-175088	Sequence 175088, A
c 37	15.8	79.0	857	4	US-09-673-395A-49	Sequence 49, Appl
c 38	15.8	79.0	2880	1	US-08-158-189-1	Sequence 1, Appl
c 39	15.8	79.0	4937	4	US-09-949-016-4121	Sequence 4121, Ap
c 40	15.8	79.0	5348	4	US-09-949-016-17509	Sequence 17509, A
c 41	15.8	79.0	5349	4	US-09-949-016-12206	Sequence 12206, A
c 42	15.8	79.0	6674	4	US-09-620-312D-110	Sequence 110, App
c 43	15.8	79.0	7292	4	US-09-949-016-14862	Sequence 14862, A
c 44	15.8	79.0	12157	4	US-09-949-016-13490	Sequence 13490, A
c 45	15.8	79.0	12157	4	US-09-949-016-13491	Sequence 13491, A
c 46	15.8	79.0	12157	4	US-09-949-016-15709	Sequence 15709, A
c 47	15.8	79.0	12157	4	US-09-949-016-15710	Sequence 15710, A
c 48	15.8	79.0	12928	4	US-09-949-016-12772	Sequence 12772, A
c 49	15.8	79.0	12929	4	US-09-949-016-16702	Sequence 16702, A
c 50	15.8	79.0	14516	4	US-09-949-016-17047	Sequence 17047, A
c 51	15.8	79.0	16056	4	US-09-949-016-16211	Sequence 16211, A
c 52	15.8	79.0	16056	4	US-09-949-016-16212	Sequence 16212, A
c 53	15.8	79.0	29771	4	US-09-949-016-12754	Sequence 12754, A
c 54	15.8	79.0	29771	4	US-09-949-016-13956	Sequence 13956, A
c 55	15.8	79.0	36820	4	US-09-949-016-16665	Sequence 16665, A
c 56	15.8	79.0	42000	4	US-10-081-563-25	Sequence 25, Appl
c 57	15.8	79.0	44676	4	US-09-949-016-17511	Sequence 17511, A
c 58	15.8	79.0	51698	4	US-09-949-016-12671	Sequence 12671, A
c 59	15.8	79.0	57507	4	US-09-949-016-15019	Sequence 15019, A
c 60	15.8	79.0	70770	4	US-09-949-016-16938	Sequence 16938, A
c 61	15.8	79.0	96340	4	US-09-949-016-15863	Sequence 15863, A
c 62	15.8	79.0	113100	4	US-09-949-016-12245	Sequence 12245, A
c 63	15.8	79.0	134140	4	US-09-949-016-12672	Sequence 12672, A
c 64	15.8	79.0	134241	4	US-09-949-016-12674	Sequence 12674, A
c 65	15.8	79.0	134242	4	US-09-949-016-15813	Sequence 15813, A
c 66	15.8	79.0	134242	4	US-09-949-016-15814	Sequence 15814, A
c 67	15.8	79.0	134242	4	US-09-949-016-15815	Sequence 15815, A
c 68	15.8	79.0	176006	4	US-09-949-016-16804	Sequence 16804, A
c 69	15.8	79.0	200663	4	US-09-949-016-12559	Sequence 12559, A
c 70	15.8	79.0	232034	4	US-09-949-016-13477	Sequence 13477, A
c 71	15.8	79.0	253375	4	US-09-949-016-12849	Sequence 12849, A
c 72	15.8	79.0	392000	4	US-10-027-983-11	Sequence 11, Appl
c 73	15.8	79.0	784019	4	US-09-949-016-14033	Sequence 14033, A
c 74	15.8	79.0	828152	4	US-09-949-016-12777	Sequence 12777, A
c 75	15.4	77.0	370	4	US-09-640-211A-1483	Sequence 1483, Ap
c 76	15.4	77.0	478	4	US-09-640-211A-218	Sequence 218, App
c 77	15.4	77.0	601	4	US-09-949-016-59777	Sequence 59777, A
c 78	15.4	77.0	601	4	US-09-949-016-59781	Sequence 59781, A
c 79	15.4	77.0	601	4	US-09-949-016-140249	Sequence 140249, A
c 80	15.4	77.0	601	4	US-09-949-016-140253	Sequence 140253, A
c 81	15.4	77.0	601	4	US-09-949-016-159914	Sequence 159914, A
c 82	15.4	77.0	601	4	US-09-949-016-159935	Sequence 159935, A
c 83	15.4	77.0	601	4	US-09-949-016-192817	Sequence 192817, A
c 84	15.4	77.0	601	4	US-09-949-016-203973	Sequence 203973, A
c 85	15.4	77.0	988	4	US-09-774-528-432	Sequence 432, App
c 86	15.4	77.0	1162	1	US-08-474-140-14	Sequence 14, Appl
c 87	15.4	77.0	1162	1	US-08-477-630-14	Sequence 14, Appl
c 88	15.4	77.0	1162	1	US-08-472-293-14	Sequence 14, Appl
c 89	15.4	77.0	1162	1	US-08-474-545-14	Sequence 14, Appl
c 90	15.4	77.0	1162	1	US-08-478-341-14	Sequence 14, Appl
c 91	15.4	77.0	1162	3	US-08-996-733-14	Sequence 14, Appl
c 92	15.4	77.0	2370	4	US-09-873-404-1	Sequence 1, Appl
c 93	15.4	77.0	2370	4	US-10-243-735-1	Sequence 1, Appl
c 94	15.4	77.0	3167	4	US-09-949-001-7	Sequence 7, Appl
c 95	15.4	77.0	3198	4	US-09-949-001-2	Sequence 2, Appl
c 96	15.4	77.0	4060	1	US-08-308-949A-1	Sequence 1, Appl
c 97	15.4	77.0	4464	1	US-08-474-140-8	Sequence 8, Appl
c 98	15.4	77.0	4464	1	US-08-474-140-9	Sequence 9, Appl
c 99	15.4	77.0	4464	1	US-08-477-630-8	Sequence 8, Appl
c 100	15.4	77.0	4464	1	US-08-477-630-9	Sequence 9, Appl

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OM nucleic - nucleic search, using sw model

Run on: July 5, 2005, 10:04:06 ; Search time 3937.44 Seconds  
(without alignments)  
31.859 Million cell updates/sec

Title: US-09-943-115A-9

Perfect score: 20

Sequence: 1 catgcccgtctctcttcta 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6313374 seqs, 3136092125 residues

Total number of hits satisfying chosen parameters: 12626748

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications NA.\*

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- 2: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*
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- 6: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*
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- 8: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09D\_PUBCOMB.seq.\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*
- 18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq.\*
- 19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq.\*
- 20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq.\*
- 21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq.\*
- 22: /cgn2\_6/ptodata/1/pubpna/US10J\_PUBCOMB.seq.\*
- 23: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq.\*
- 24: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq.\*
- 25: /cgn2\_6/ptodata/1/pubpna/US11B\_PUBCOMB.seq.\*
- 26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	10	US-09-943-115A-9
2	20	100.0	1345	14	US-09-943-115A-1
3	20	100.0	1345	14	US-10-146-575-3
4	20	100.0	1345	14	US-10-085-612-3
5	20	100.0	12983	21	US-10-435-607-1
6	20	100.0	13035	15	US-10-121-960C-14
7	20	100.0	15185	15	US-10-121-960C-17

20	100.0	96960	21	US-10-484-577-662	Sequence 662, App
17	85.0	1025	9	US-09-822-849A-144	Sequence 144, App
16.8	84.0	192	8	US-08-781-986A-1551	Sequence 1551, App
16.8	84.0	192	18	US-10-329-624-1551	Sequence 219495, App
16.8	84.0	611	13	US-10-027-632-219495	Sequence 219495, App
16.8	84.0	611	17	US-10-027-632-219495	Sequence 219495, App
16.8	84.0	646	13	US-10-027-632-247126	Sequence 247126, App
16.8	84.0	646	17	US-10-027-632-247126	Sequence 247126, App
16.8	84.0	1071	13	US-10-027-632-256517	Sequence 256517, App
16.8	84.0	1071	13	US-10-027-632-256518	Sequence 256518, App
16.8	84.0	1071	17	US-10-027-632-256517	Sequence 256517, App
16.8	84.0	1071	17	US-10-027-632-256518	Sequence 256518, App
16.8	84.0	2122	18	US-10-424-599-119619	Sequence 119619, App
16.8	84.0	33988	19	US-10-741-601-5670	Sequence 5670, App
16.8	84.0	33988	19	US-10-741-600-17701	Sequence 17701, App
16.8	84.0	37135	18	US-10-052-482-151	Sequence 151, App
16.8	84.0	87687	13	US-10-087-192-1978	Sequence 1978, App
16.8	84.0	138	20	US-10-357-930-15544	Sequence 15544, App
16.4	82.0	177	17	US-10-242-535A-15202	Sequence 15202, App
16.4	82.0	177	18	US-10-085-783A-15202	Sequence 15202, App
16.4	82.0	228	9	US-09-783-590-176	Sequence 176, App
16.4	82.0	245	20	US-10-357-930-6375	Sequence 6375, App
16.4	82.0	382	17	US-10-242-535A-36128	Sequence 36128, App
16.4	82.0	382	18	US-10-085-783A-36128	Sequence 36128, App
16.4	82.0	549	13	US-10-027-632-51536	Sequence 51536, App
16.4	82.0	549	13	US-10-027-632-51537	Sequence 51537, App
16.4	82.0	549	13	US-10-027-632-53794	Sequence 53794, App
16.4	82.0	549	17	US-10-027-632-53795	Sequence 53795, App
16.4	82.0	549	13	US-10-027-632-321440	Sequence 321440, App
16.4	82.0	549	13	US-10-027-632-321441	Sequence 321441, App
16.4	82.0	549	17	US-10-027-632-321441	Sequence 321441, App
16.4	82.0	556	20	US-10-357-930-36361	Sequence 36361, App
16.4	82.0	556	20	US-10-357-930-45393	Sequence 45393, App
16.4	82.0	565	14	US-10-060-036-4338	Sequence 4338, App
16.4	82.0	791	20	US-10-357-930-24064	Sequence 24064, App
16.4	82.0	791	20	US-10-357-930-29974	Sequence 29974, App
16.4	82.0	820	17	US-10-027-632-154192	Sequence 154192, App
16.4	82.0	820	17	US-10-027-632-154192	Sequence 154192, App
16.4	82.0	820	17	US-10-027-632-154192	Sequence 154192, App
16.4	82.0	2164	19	US-10-648-593-30	Sequence 30, Appl
16.4	82.0	2432	13	US-10-027-632-103097	Sequence 103097, App
16.4	82.0	2432	13	US-10-027-632-111848	Sequence 111848, App
16.4	82.0	2432	17	US-10-027-632-103097	Sequence 103097, App
16.4	82.0	2432	17	US-10-027-632-111848	Sequence 111848, App
16.4	82.0	2749	9	US-09-822-849A-399	Sequence 399, App
16.4	82.0	2905	15	US-10-037-270-45	Sequence 45, Appl
16.4	82.0	2905	17	US-10-117-722-45	Sequence 45, Appl
16.4	82.0	3543	10	US-09-783-732-1	Sequence 1, Appl
16.4	82.0	3543	10	US-09-783-732-1	Sequence 1, Appl
16.4	82.0	3550	21	US-10-956-157-4290	Sequence 4290, App
16.4	82.0	3650	21	US-09-783-732-3	Sequence 3, Appl
16.4	82.0	3655	21	US-10-489-740-107	Sequence 107, App
16.4	82.0	3655	21	US-10-956-157-2109	Sequence 2109, App
16.4	82.0	3655	21	US-10-956-157-2109	Sequence 2109, App
16.4	82.0	16552	9	US-09-764-855-321	Sequence 321, App
16.4	82.0	16552	9	US-09-764-855-321	Sequence 321, App
16.4	82.0	16552	14	US-10-072-349-321	Sequence 321, App
16.4	82.0	16552	14	US-10-072-349-321	Sequence 321, App
16.4	82.0	144179	13	US-10-087-192-511	Sequence 511, App
16.4	82.0	319608	17	US-10-147-603-1	GENERAL INFORMATI
16.4	82.0	518360	19	US-10-367-094-125	Sequence 125, App
16.4	82.0	518360	19	US-10-367-094-125	Sequence 125, App
16	80.0	181	18	US-10-424-599-35871	Sequence 35871, App
16	80.0	363	14	US-10-293-705-1	Sequence 1, Appl
16	80.0	363	20	US-10-779-267-1	Sequence 1, Appl
16	80.0	570	17	US-10-305-720-47	Sequence 47, Appl
16	80.0	16998	21	US-10-741-600-19798	Sequence 19798, App
16	80.0	30431	21	US-10-741-600-17746	Sequence 17746, App
16	80.0	2047	18	US-10-424-599-123925	Sequence 123925, App
15.8	79.0	217	18	US-09-783-590-7843	Sequence 7843, App
15.8	79.0	250	9	US-09-764-872-522	Sequence 522, App
15.8	79.0	329	10	US-09-814-353-20450	Sequence 20450, App
15.8	79.0	392	10	US-09-814-353-20450	Sequence 20450, App

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OM nucleic - nucleic search, using sw model

Run on: July 5, 2005, 09:16:41 ; Search time 951.949 Seconds  
(without alignments)  
967.120 Million cell updates/sec

Title: US-09-943-115A-10

Perfect score: 19

Sequence: 1 ccatcccttcgcaatc 19

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_htg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	19	6	AX421262 Sequence
C 2	19	100.0	1013	6	AF181105 Homo sapi
C 3	19	100.0	1345	6	AR142139 Sequence
C 4	19	100.0	1345	6	AR142140 Sequence
C 5	19	100.0	1345	6	BD222974 CYP3A4 NF
C 6	19	100.0	1345	6	BD222975 CYP3A4 NF
C 7	19	100.0	1345	6	CQ776018 Sequence
C 8	19	100.0	1345	6	CQ790615 Sequence
C 9	19	100.0	1345	6	AR222893 Sequence
C 10	19	100.0	1345	6	AX421253 Sequence
C 11	19	100.0	1345	9	HUMCYP3A4
C 12	19	100.0	6101	6	CQ806643 Sequence
C 13	19	100.0	11374	9	AF185589 Homo sapi
C 14	19	100.0	96960	6	AX706964 Sequence
C 15	19	100.0	96960	6	AX707894 Sequence
C 16	19	100.0	123778	9	AC069294 Homo sapi
C 17	19	100.0	170470	9	AC146392 Pan trogl
C 18	19	100.0	174832	9	AF280107 Homo sapi
C 19	17.4	91.6	1652	8	AY598939 Aspergill

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OM nucleic - nucleic search, using sw model

Run on: July 5, 2005, 10:04:06 ; Search time 3740.56 Seconds  
(without alignments)  
31.859 Million cell updates/sec

Title: US-09-943-115A-10

Perfect score: 19

Sequence: 1 ccatcccttcgcaatc 19

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 6313374 seqs, 3136092125 residues

Total number of hits satisfying chosen parameters: 12626748

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match: 0%

Maximum Match: 100%

Listing first 1000 summaries

Database : Published Applications NA.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	19	10	US-09-943-115A-10
2	19	100.0	1345	10	US-09-943-115A-10
3	19	100.0	1345	14	US-10-146-575-3
4	19	100.0	1345	14	US-10-085-612-3
5	19	100.0	12983	21	US-10-415-607-1
6	19	100.0	13035	15	US-10-121-960C-14
7	19	100.0	15185	15	US-10-121-960C-17

Sequence 662, App	US-10-484-577-662	21	96960	100.0	19
Sequence 4240, App	US-10-106-698-4240	15	309	86.3	16.4
Sequence 39686, A	US-10-027-632-39686	13	460	86.3	16.4
Sequence 39686, A	US-10-027-632-39686	13	460	86.3	16.4
Sequence 8303, App	US-10-029-386-8303	16	520	86.3	16.4
Sequence 39434, A	US-10-027-632-39434	13	568	86.3	16.4
Sequence 39435, A	US-10-027-632-39435	13	568	86.3	16.4
Sequence 39434, A	US-10-027-632-39434	13	568	86.3	16.4
Sequence 39435, A	US-10-027-632-39435	13	568	86.3	16.4
Sequence 4, Appli	US-09-957-997-4	9	1012	86.3	16.4
Sequence 47, Appli	US-10-257-166-47	17	8943	86.3	16.4
Sequence 1, Appli	US-09-957-997-1	9	8943	86.3	16.4
Sequence 4, Appli	US-10-415-607-4	21	11186	86.3	16.4
Sequence 1000, App	US-10-087-192-1000	13	256493	86.3	16.4
Sequence 67010, App	US-10-425-115-67010	20	810	84.2	16
Sequence 28486, A	US-10-425-115-28486	18	1036	84.2	16
Sequence 67013, A	US-10-425-115-67013	20	1036	84.2	16
Sequence 67012, A	US-10-425-115-67012	20	1146	84.2	16
Sequence 128026, A	US-10-425-115-128026	20	369	83.2	15.8
Sequence 10968, A	US-10-767-701-10968	19	416	83.2	15.8
Sequence 122852, A	US-10-424-599-122852	18	421	83.2	15.8
Sequence 436, App	US-09-954-456-436	9	446	83.2	15.8
Sequence 2188, App	US-09-954-456-2188	9	446	83.2	15.8
Sequence 273, App	US-09-967-768A-273	9	446	83.2	15.8
Sequence 3463, App	US-10-843-641A-3463	21	446	83.2	15.8
Sequence 5215, App	US-10-843-641A-5215	21	446	83.2	15.8
Sequence 6418, App	US-10-843-641A-6418	21	446	83.2	15.8
Sequence 61363, A	US-10-437-963-61363	19	489	83.2	15.8
Sequence 192971, A	US-10-425-115-192971	20	490	83.2	15.8
Sequence 172, App	US-09-833-790-172	9	501	83.2	15.8
Sequence 133809, A	US-10-027-632-133809	13	520	83.2	15.8
Sequence 133810, A	US-10-027-632-133810	13	520	83.2	15.8
Sequence 133811, A	US-10-027-632-133811	13	520	83.2	15.8
Sequence 133809, A	US-10-027-632-133809	13	520	83.2	15.8
Sequence 133810, A	US-10-027-632-133810	13	520	83.2	15.8
Sequence 133811, A	US-10-027-632-133811	13	520	83.2	15.8
Sequence 133812, A	US-10-027-632-133812	13	520	83.2	15.8
Sequence 151802, A	US-10-027-632-151802	17	747	83.2	15.8
Sequence 151802, A	US-10-027-632-151802	17	747	83.2	15.8
Sequence 12875, A	US-10-357-930-12875	20	752	83.2	15.8
Sequence 136499, A	US-10-027-632-136499	13	835	83.2	15.8
Sequence 136500, A	US-10-027-632-136500	13	835	83.2	15.8
Sequence 13354, A	US-10-027-632-13354	17	835	83.2	15.8
Sequence 41894, A	US-10-425-115-41894	20	1119	83.2	15.8
Sequence 10967, A	US-10-767-701-10967	19	1395	83.2	15.8
Sequence 1132, App	US-10-094-749-1132	17	2214	83.2	15.8
Sequence 74913, A	US-10-437-963-74913	19	4205	83.2	15.8
Sequence 1999, App	US-10-087-192-1999	13	5840	83.2	15.8
Sequence 18185, A	US-10-437-963-18185	19	680	81.1	15.4
Sequence 17866, A	US-10-425-114-17866	18	785	81.1	15.4
Sequence 17877, A	US-10-425-114-17877	18	785	81.1	15.4
Sequence 122215, A	US-10-027-632-122215	13	870	81.1	15.4
Sequence 122215, A	US-10-027-632-122215	13	870	81.1	15.4
Sequence 118796, A	US-10-027-632-118796	17	1000	81.1	15.4
Sequence 121793, A	US-10-027-632-121793	17	1000	81.1	15.4
Sequence 121794, A	US-10-027-632-121794	13	1002	81.1	15.4
Sequence 121795, A	US-10-027-632-121795	13	1002	81.1	15.4
Sequence 121793, A	US-10-027-632-121793	13	1002	81.1	15.4
Sequence 121794, A	US-10-027-632-121794	13	1002	81.1	15.4
Sequence 121795, A	US-10-027-632-121795	13	1002	81.1	15.4
Sequence 121793, A	US-10-027-632-121793	13	1002	81.1	15.4
Sequence 121794, A	US-10-027-632-121794	13	1002	81.1	15.4
Sequence 121795, A	US-10-027-632-121795	13	1002	81.1	15.4
Sequence 23518, A	US-10-424-599-23518	17	1102	81.1	15.4
Sequence 7998, App	US-10-425-114-7998	18	1974	81.1	15.4
Sequence 29365, A	US-10-425-115-29365	20	2024	81.1	15.4
Sequence 30885, A	US-10-282-122A-30885	17	2139	81.1	15.4
Sequence 25, Appli	US-10-454-199-25	17	2380	81.1	15.4
Sequence 23374, A	US-10-437-963-23374	19	2940	81.1	15.4
Sequence 23519, A	US-10-424-599-23519	18	4059	81.1	15.4
Sequence 3, Appli	US-10-025-187-3	13	45839	81.1	15.4



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OM nucleic - nucleic search, using sw model

Run on: July 5, 2005, 09:16:41 ; Search time 96.4615 Seconds  
(without alignments)  
322.297 Million cell updates/sec

Title: US-09-943-115A-10

Perfect score: 19

Sequence: 1 ccattcccttcgcaatc 19

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 1000 summaries

Database : Issued Patents NA.\*  
1: /cgn2\_6/ptodata/1/ina/5A-COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5B-COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A-COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B-COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS-COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	19	100.0	1345	3	US-09-372-339-1
C 2	19	100.0	1345	3	US-09-372-339-2
C 3	19	100.0	1345	3	US-09-144-367-3
C 4	19	100.0	31197	4	US-09-949-016-12963
C 5	19	100.0	103934	4	US-09-949-016-14433
C 6	16.4	85.3	34172	4	US-09-949-016-14432
C 7	15.8	83.2	389	4	US-09-513-999C-21877
C 8	15.8	83.2	594	4	US-09-134-000C-2075
C 9	15.8	83.2	663	4	US-09-902-540-1693
C 10	15.8	83.2	73757	4	US-09-949-016-15369
C 11	15.4	81.1	601	4	US-09-949-016-89049
C 12	15.4	81.1	2380	4	US-09-436-699C-25
C 13	15.4	81.1	9649	4	US-09-949-016-15672
C 14	15.4	81.1	27317	4	US-09-949-016-14955
C 15	15.4	81.1	49399	4	US-09-949-016-13780
C 16	15.4	81.1	162465	4	US-09-949-016-14264
C 17	15	78.9	882	4	US-09-489-039A-2691
C 18	15	78.9	1389	4	US-09-351-150A-22
C 19	15	78.9	8841	4	US-09-949-016-14996
C 20	15	78.9	11668	4	US-09-949-016-11878
C 21	15	78.9	11713	4	US-09-949-016-13554
C 22	15	78.9	24494	4	US-09-351-150A-1
C 23	14.8	77.9	246	4	US-09-248-796A-10333
C 24	14.8	77.9	546	4	US-09-902-540-5427
C 25	14.8	77.9	548	4	US-09-573-080A-268
C 26	14.8	77.9	601	4	US-09-949-016-48798
C 27	14.8	77.9	601	4	US-09-949-016-48970

C 28	14.8	77.9	601	4	US-09-949-016-49142	Sequence 49142, A
C 29	14.8	77.9	601	4	US-09-949-016-49318	Sequence 49318, A
C 30	14.8	77.9	601	4	US-09-949-016-89071	Sequence 89071, A
C 31	14.8	77.9	601	4	US-09-949-016-167922	Sequence 167922, A
C 32	14.8	77.9	601	4	US-09-949-016-167923	Sequence 167923, A
C 33	14.8	77.9	601	4	US-09-949-016-167924	Sequence 167924, A
C 34	14.8	77.9	601	4	US-09-949-016-189898	Sequence 189898, A
C 35	14.8	77.9	629	4	US-09-513-999C-11622	Sequence 11622, A
C 36	14.8	77.9	1002	4	US-09-252-991A-11872	Sequence 11872, A
C 37	14.8	77.9	1230	4	US-09-252-991A-4767	Sequence 4767, Ap
C 38	14.8	77.9	1356	4	US-09-252-991A-4740	Sequence 4740, Ap
C 39	14.8	77.9	1394	3	US-09-149-476-101	Sequence 101, Ap
C 40	14.8	77.9	1464	4	US-09-252-991A-11508	Sequence 11508, A
C 41	14.8	77.9	1629	4	US-09-252-991A-11733	Sequence 11733, A
C 42	14.8	77.9	5246	4	US-09-799-451-474	Sequence 474, Ap
C 43	14.8	77.9	34953	4	US-09-902-540-1263	Sequence 1263, Ap
C 44	14.8	77.9	35784	4	US-09-949-016-16785	Sequence 16785, A
C 45	14.8	77.9	35784	4	US-09-949-016-16786	Sequence 16786, A
C 46	14.8	77.9	85122	4	US-09-949-016-14693	Sequence 14693, A
C 47	14.8	77.9	119214	4	US-09-949-016-12507	Sequence 12507, A
C 48	14.8	77.9	141560	4	US-09-949-016-16476	Sequence 16476, A
C 49	14.8	77.9	183112	4	US-09-949-016-14184	Sequence 14184, A
C 50	14.8	77.9	227750	4	US-09-949-016-17175	Sequence 17175, A
C 51	14.8	77.9	251769	4	US-09-949-016-13185	Sequence 13185, A
C 52	14.8	77.9	251769	4	US-09-949-016-13186	Sequence 13186, A
C 53	14.8	77.9	266748	4	US-09-949-016-13187	Sequence 13187, A
C 54	14.8	77.9	266748	4	US-09-949-016-13188	Sequence 13188, A
C 55	14.8	77.9	285986	4	US-09-949-016-12287	Sequence 12287, A
C 56	14.8	77.9	288031	4	US-09-949-016-14864	Sequence 14864, A
C 57	14.4	75.8	601	4	US-09-949-016-200201	Sequence 200201, A
C 58	14.4	75.8	605	3	US-08-630-915A-5	Sequence 5, Appli
C 59	14.4	75.8	605	4	US-09-879-957-5	Sequence 5, Appli
C 60	14.4	75.8	1053	4	US-09-902-540-2666	Sequence 2666, Ap
C 61	14.4	75.8	1230	4	US-09-902-540-7025	Sequence 7025, Ap
C 62	14.4	75.8	1914	4	US-09-540-236-1278	Sequence 1278, Ap
C 63	14.4	75.8	2226	4	US-09-949-016-4853	Sequence 4853, Ap
C 64	14.4	75.8	2256	4	US-09-540-236-400	Sequence 400, App
C 65	14.4	75.8	2449	4	US-09-710-279-2947	Sequence 2947, Ap
C 66	14.4	75.8	2661	3	US-09-134-001C-1659	Sequence 1659, Ap
C 67	14.4	75.8	2826	4	US-09-695-481-1	Sequence 1, Appli
C 68	14.4	75.8	2925	4	US-09-695-481-3	Sequence 3, Appli
C 69	14.4	75.8	3049	4	US-09-710-279-4151	Sequence 4151, Ap
C 70	14.4	75.8	3063	4	US-09-799-451-511	Sequence 511, App
C 71	14.4	75.8	3282	1	US-08-072-574-11	Sequence 11, Appl
C 72	14.4	75.8	3282	1	US-08-486-270-11	Sequence 11, Appl
C 73	14.4	75.8	3282	3	US-08-367-264-11	Sequence 11, Appl
C 74	14.4	75.8	3282	3	US-09-153-757-11	Sequence 11, Appl
C 75	14.4	75.8	3282	4	US-09-459-715-11	Sequence 11, Appl
C 76	14.4	75.8	3371	4	US-09-710-279-3490	Sequence 3490, Ap
C 77	14.4	75.8	4078	4	US-09-016-434-1133	Sequence 1133, Ap
C 78	14.4	75.8	4085	1	US-08-072-574-7	Sequence 7, Appli
C 79	14.4	75.8	4085	1	US-08-486-270-7	Sequence 7, Appli
C 80	14.4	75.8	4085	3	US-08-367-264-7	Sequence 7, Appli
C 81	14.4	75.8	4085	3	US-09-153-757-7	Sequence 7, Appli
C 82	14.4	75.8	4085	4	US-09-459-715-7	Sequence 7, Appli
C 83	14.4	75.8	4181	1	US-08-072-574-9	Sequence 9, Appli
C 84	14.4	75.8	4181	1	US-08-486-270-9	Sequence 9, Appli
C 85	14.4	75.8	4181	3	US-08-367-264-9	Sequence 9, Appli
C 86	14.4	75.8	4181	3	US-09-153-757-9	Sequence 9, Appli
C 87	14.4	75.8	4181	4	US-09-459-715-9	Sequence 9, Appli
C 88	14.4	75.8	4207	3	US-08-660-148-1	Sequence 1, Appli
C 89	14.4	75.8	4207	3	US-08-660-148-3	Sequence 3, Appli
C 90	14.4	75.8	4303	3	US-08-660-148-4	Sequence 4, Appli
C 91	14.4	75.8	4303	3	US-08-660-148-6	Sequence 6, Appli
C 92	14.4	75.8	4627	4	US-09-949-016-5553	Sequence 5553, Ap
C 93	14.4	75.8	4919	4	US-09-949-016-999	Sequence 999, App
C 94	14.4	75.8	5588	4	US-09-902-540-621	Sequence 621, App
C 95	14.4	75.8	12061	4	US-09-949-016-16134	Sequence 16134, A
C 96	14.4	75.8	13205	4	US-09-835-811-3	Sequence 3, Appli
C 97	14.4	75.8	13706	4	US-09-902-540-1124	Sequence 1124, Ap
C 98	14.4	75.8	20608	4	US-09-949-016-16595	Sequence 16595, A
C 99	14.4	75.8	50453	4	US-09-949-016-16642	Sequence 16642, A
C 100	14.4	75.8	51242	4	US-09-949-016-12486	Sequence 12486, A



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OM nucleic - nucleic search, using sw model

Run on: July 5, 2005, 09:16:41 ; Search time 2509.95 Seconds  
(without alignments)  
288.142 Million cell updates/sec

Title: US-09-943-115A-10

Perfect score: 19

Sequence: 1 ccatcccttcgaatc 19

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

EST:

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_hic:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gse1:\*

9: gb\_gse2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17.4	91.6	407	8	AZ425215 1M0205N08
2	17.4	91.6	522	8	AZ208099 SP_0136 B
3	17.4	91.6	675	7	CO196969 GEO1_3_A1
4	17.4	91.6	720	9	CR080967 Reverse_s
5	17.4	91.6	731	7	CF677590 CCAPB13TR
6	17.4	91.6	746	7	CO196968 GEO1_3_A0
7	17.4	91.6	776	7	CO158541 FL01_7_C0
8	17.4	91.6	897	7	CF690372 CCADBE67TR
9	17.4	91.6	909	7	CN783648 EST782339
10	17	89.5	297	2	BB242153 BB242153
11	17	89.5	553	2	AW223646 EST300457
12	17	89.5	573	2	AW223655 EST300466
13	17	89.5	796	7	CV497664 61883.1 M
14	16.4	86.3	180	4	BG954268 CM4-CT066
15	16.4	86.3	370	9	CL249146 ZMMBB059
16	16.4	86.3	427	8	BH872947 BP09e09.b
17	16.4	86.3	443	2	BB856031 BB856031
18	16.4	86.3	533	7	CN284843 CN284843
19	16.4	86.3	552	5	BUB16135 N061A11 P
20	16.4	86.3	555	7	CO682917 DG11-161b
21	16.4	86.3	566	7	CO680769 DG11-120h
22	16.4	86.3	603	7	CO680831 DG11-1219
23	16.4	86.3	613	7	CO689219 DG11-256g
24	16.4	86.3	642	9	CE256161 tigr-988-

C	25	16.4	86.3	688	4	BG854956
	26	16.4	86.3	717	8	BZ026281
	27	16.4	86.3	723	9	AG556684
	28	16.4	86.3	746	8	BH920535
	29	16.4	86.3	773	5	BM071866
	30	16.4	86.3	784	8	BZ078746
C	31	16.4	86.3	795	6	CD781339
	32	16.4	86.3	830	7	CV107995
C	33	16.4	86.3	860	9	CC810943
	34	16.4	86.3	972	4	BG754964
C	35	16.4	86.3	1295	4	BG754964
	36	16	84.2	115	5	BG754964
C	37	16	84.2	115	5	BG754964
	38	16	84.2	239	5	BG754964
C	39	16	84.2	242	5	BG754964
	40	16	84.2	280	4	BG754964
C	41	16	84.2	324	4	BG754964
	42	16	84.2	384	6	BG754964
C	43	16	84.2	448	1	BG754964
	44	16	84.2	455	5	BG754964
C	45	16	84.2	460	5	BG754964
	46	16	84.2	519	5	BG754964
C	47	16	84.2	520	5	BG754964
	48	16	84.2	551	6	BG754964
C	49	16	84.2	588	6	BG754964
	50	16	84.2	601	5	BG754964
C	51	16	84.2	602	9	BG754964
	52	16	84.2	687	9	BG754964
C	53	16	84.2	736	8	BG754964
	54	16	84.2	972	3	BG754964
C	55	15.8	83.2	180	1	BG754964
	56	15.8	83.2	225	2	BG754964
C	57	15.8	83.2	239	5	BG754964
	58	15.8	83.2	239	5	BG754964
C	59	15.8	83.2	250	5	BG754964
	60	15.8	83.2	257	2	BG754964
C	61	15.8	83.2	260	2	BG754964
	62	15.8	83.2	264	9	BG754964
C	63	15.8	83.2	266	2	BG754964
	64	15.8	83.2	270	8	BG754964
C	65	15.8	83.2	274	8	BG754964
	66	15.8	83.2	283	2	BG754964
C	67	15.8	83.2	300	2	BG754964
	68	15.8	83.2	310	2	BG754964
C	69	15.8	83.2	313	2	BG754964
	70	15.8	83.2	316	1	BG754964
C	71	15.8	83.2	328	7	BG754964
	72	15.8	83.2	349	4	BG754964
C	73	15.8	83.2	360	1	BG754964
	74	15.8	83.2	380	6	BG754964
C	75	15.8	83.2	382	6	BG754964
	76	15.8	83.2	384	9	BG754964
C	77	15.8	83.2	393	4	BG754964
	78	15.8	83.2	397	9	BG754964
C	79	15.8	83.2	403	8	BG754964
	80	15.8	83.2	403	8	BG754964
C	81	15.8	83.2	404	2	BG754964
	82	15.8	83.2	410	2	BG754964
C	83	15.8	83.2	413	6	BG754964
	84	15.8	83.2	416	5	BG754964
C	85	15.8	83.2	419	4	BG754964
	86	15.8	83.2	423	5	BG754964
C	87	15.8	83.2	423	4	BG754964
	88	15.8	83.2	431	1	BG754964
C	89	15.8	83.2	446	8	BG754964
	90	15.8	83.2	450	4	BG754964
C	91	15.8	83.2	452	4	BG754964
	92	15.8	83.2	454	8	BG754964
C	93	15.8	83.2	454	8	BG754964
	94	15.8	83.2	457	4	BG754964
C	95	15.8	83.2	460	8	BG754964
	96	15.8	83.2	461	2	BG754964
C	97	15.8	83.2	464	5	BG754964

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OM nucleic - nucleic search, using sw model

Run on: July 5, 2005, 09:16:41 ; Search time 329.333 Seconds  
(without alignments)  
341.524 Million cell updates/sec

Title: US-09-943-115A-10  
Perfect score: 19  
Sequence: 1 ccattcccttcgaatc 19

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : N\_Geneseq\_16Dec04:\*  
1: Geneseqn1980as:\*  
2: Geneseqn1990as:\*  
3: Geneseqn2000as:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002as:\*  
7: Geneseqn2002bs:\*  
8: Geneseqn2003as:\*  
9: Geneseqn2003bs:\*  
10: Geneseqn2003cs:\*  
11: Geneseqn2003ds:\*  
12: Geneseqn2004as:\*  
13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	19	6	ABK68754 PCR prime
2	19	100.0	1345	2	AAX28296 Human CYP
3	19	100.0	1345	2	AAX28296 Human CYP
4	19	100.0	1345	3	AAX257019 Nucleic a
5	19	100.0	1345	3	AAX257020 Nucleic a
6	19	100.0	1345	6	ABK68745 5'-flanki
7	19	100.0	1345	12	ADJ84441 Human phe
8	19	100.0	6101	13	ADS89077 Human CYP
9	19	100.0	12983	6	AD41239 Human CYP
10	19	100.0	13035	8	AD51997 Human CYP
11	19	100.0	15185	8	AD52000 Human CYP
12	19	100.0	39071	12	ADM97420 Prostata
13	19	100.0	96960	8	ACF62734 Cancer ba
14	19	100.0	96960	8	ADB20849 MRPL-base
15	19	100.0	96960	10	ADB87938 Human UGT
16	19	100.0	96960	10	ADB96921 Human MDR
17	19	100.0	96960	10	ADB92112 Human MDR
18	19	100.0	123785	10	ABX77171 DNA seque
19	17.4	91.6	6101	13	ADS89689 Oligonuc
20	17.4	91.6	6101	13	ADS89415 Oligonuc
21	16.4	86.3	309	4	AAX37148 Human col

21	16.4	86.3	520	12	ACH75108	Ach75108 Human gen
22	16.4	86.3	1012	6	AAD36215	Aad36215 Human pro
23	16.4	86.3	7966	4	ABL19154	Ab119154 Drosophil
24	16.4	86.3	8943	6	ABK39966	Abk39966 Humar che
25	16.4	86.3	9903	4	ABL09916	Ab109916 Drosophil
26	16.4	86.3	11186	6	AAD1242	Aad1242 Human CYP
27	16.4	86.3	11186	6	AAD36213	Aad36213 Human CYP
28	16.4	86.3	256493	11	ACN44514	Acn44514 Human gen
29	16.4	84.2	812	2	AAX16385	Aax16385 Human gen
30	15.8	83.2	389	3	AAC17802	Aac17802 Human sec
31	15.8	83.2	446	6	ABL68081	Ab168081 Ovary can
32	15.8	83.2	446	6	ABL65126	Ab165126 Lung can
33	15.8	83.2	446	6	ABL66878	Ab166878 Lung can
34	15.8	83.2	446	6	ABT11074	Abt11074 Human bre
35	15.8	83.2	501	6	AAS61631	Aas61631 Lung smal
36	15.8	83.2	542	4	AAS44754	Aas44754 Human con
37	15.8	83.2	567	12	ADQ81633	Adq81633 Enterococ
38	15.8	83.2	567	12	ADQ81635	Adq81635 Enterococ
39	15.8	83.2	594	10	ADH84190	Adh84190 Enterococ
40	15.8	83.2	752	5	ABV12884	Abv12884 Human pro
41	15.8	83.2	1717	4	AAS44582	Aas44582 Human ful
42	15.8	83.2	1990	10	ADA52447	Ada52447 Human cod
43	15.8	83.2	2214	10	ADA53564	Ada53564 Human cod
44	15.8	83.2	2470	4	AAH16228	Aah16228 Human CDN
45	15.8	83.2	2686	5	AAS73640	Aas73640 DNA encod
46	15.8	83.2	3134	12	ADQ87636	Adq87636 Human tum
47	15.8	83.2	5840	2	AAX12968	Aax12968 Enterococ
48	15.8	83.2	5840	6	ABS98763	Abs98763 Enterococ
49	15.8	83.2	185555	11	ACN45180	Acn45180 Mouse gen
50	15.4	81.1	253	12	ADP99569	Adp99569 Nicotiana
51	15.4	81.1	323	8	ABS57436	Abs57436 Metalloth
52	15.4	81.1	330	8	ABZ56354	Abz56354 Aspergill
53	15.4	81.1	2139	8	ACA43015	Aca43015 Prokaryot
54	15.4	81.1	2380	12	ADI19357	Adi19357 Soybean t
55	15.4	81.1	2380	12	ADJ65942	Adj65942 soybean t
56	15.4	81.1	3018	8	ADA70619	Ada70619 Rice gene
57	15.4	81.1	4821	4	AAH62756	Aah62756 Shrimp wh
58	15.4	81.1	5872	4	ABL06090	Ab106090 Drosophil
59	15.4	81.1	45839	6	AAD42191	Aad42191 Human rgtv
60	15.4	81.1	77425	6	ABK83502	Abk83502 Human CDN
61	15.4	81.1	110000	10	ADG70184	Adg70184 DNA of BA
62	15.4	81.1	175338	11	ACN45088	Acn45088 Mouse gen
63	15.4	81.1	188794	12	ADQ59476	Adq59476 Human can
64	15.4	81.1	305107	4	AAH62689	Aah62689 Shrimp wh
65	15.4	81.1	349981	10	ADC87619	Adc87619 Human GPC
66	15	78.9	447	3	AAA60920	Aaa60920 Phaneroch
67	15	78.9	882	11	ACH96896	Ach96896 Klebsiell
68	15	78.9	1230	3	AAH13712	Aah13712 Human pro
69	15	78.9	1389	3	AAZ91264	Aaz91264 Fumarate
70	15	78.9	2380	3	AAV07911	Aav07911 Mouse cys
71	15	78.9	2381	2	AAV07911	Aav07911 Mouse cys
72	15	78.9	24494	3	AAZ91253	Aaz91253 Bacterium
73	14.8	77.9	31	4	AAI30350	Aai30350 Human ein
74	14.8	77.9	139	12	ACH86962	Ach86962 Human gen
75	14.8	77.9	259	12	ADQ05883	Adq05883 Soybean t
76	14.8	77.9	321	6	ABK73598	Abk73598 Bacillus
77	14.8	77.9	402	4	AAI84778	Aai84778 Human pol
78	14.8	77.9	402	9	ACH49084	Ach49084 Human leu
79	14.8	77.9	461	9	ACH27948	Ach27948 Human adu
80	14.8	77.9	482	9	ACH27904	Ach27904 Human adu
81	14.8	77.9	513	6	ABK70158	Abk70158 Human lun
82	14.8	77.9	548	7	ADS31235	Ads31235 Human gen
83	14.8	77.9	578	6	ABL36882	Ab136882 Human col
84	14.8	77.9	581	12	ACH73231	Ach73231 Human gen
85	14.8	77.9	583	13	AD864038	Adr64038 Corton cd
86	14.8	77.9	601	12	ADL15860	Adl15860 Novel tra
87	14.8	77.9	616	8	ACA45195	Aca45195 Prokaryot
88	14.8	77.9	616	12	ADQ09663	Adq09663 Rice 13kd
89	14.8	77.9	629	3	AAC07547	Aac07547 Human sec
90	14.8	77.9	638	8	ABZ53978	Abz53978 Aspergill
91	14.8	77.9	862	6	ABQ46057	Abq46057 Oligonuc
92	14.8	77.9	862	6	ABQ46056	Abq46056 Oligonuc
93	14.8	77.9	869	12	ADJ40322	Adj40322 Plant cDN